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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/833,017

DATE: 10/10/2001

TIME: 10:13:19

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF3\10102001\I833017.raw

3 <110> APPLICANT: CVITKOVITCH, Dennis
5 <120> TITLE OF INVENTION: SIGNAL PEPTIDES NUCLEIC ACID MOLECULES AND METHODS FOR
TREATMENT

6 OF CRIES
8 <130> FILE REFERENCE: P04885US1
10 <140> CURRENT APPLICATION NUMBER: 09/833,017
12 <141> CURRENT FILING DATE: 2001-04-10
14 <150> PRIOR APPLICATION NUMBER: PCT/CA00/00605
15 <151> PRIOR FILING DATE: 2000-05-25
17 <150> PRIOR APPLICATION NUMBER: 2,302,861
18 <151> PRIOR FILING DATE: 2000-04-10
20 <150> PRIOR APPLICATION NUMBER: 2,332,733
21 <151> PRIOR FILING DATE: 2001-02-20
23 <160> NUMBER OF SEQ ID NOS: 28
25 <170> SOFTWARE: PatentIn version 3.0
27 <210> SEQ ID NO: 1
29 <211> LENGTH: 141
31 <212> TYPE: DNA
33 <213> ORGANISM: Streptococcus mutans
35 <220> FEATURE:
37 <221> NAME/KEY: CDS
39 <222> LOCATION: (1)..(141)
41 <400> SEQUENCE: 1

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43 Met Lys Lys Thr Leu Ser Leu Lys Asn Asp Phe Lys Glu Ile Lys Thr
44 1 5 10 15
46 gat gaa tta gag att atc att ggc gga agc gga agc cta tca aca ttt 96
47 Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
48 20 25 30
50 ttc cgg ctg ttt aac aga agt ttt aca caa gct ttg gga aaa taa 141
51 Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
52 35 40 45

55 <210> SEQ ID NO: 2
57 <211> LENGTH: 46
59 <212> TYPE: PRT
61 <213> ORGANISM: Streptococcus mutans
65 <400> SEQUENCE: 2
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68 1 5 10 15
71 Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
72 20 25 30
75 Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
76 35 40 45
79 <210> SEQ ID NO: 3
81 <211> LENGTH: 1326
83 <212> TYPE: DNA
85 <213> ORGANISM: Streptococcus mutans
89 <220> FEATURE:

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91 <221> NAME/KEY: CDS

93 <222> LOCATION: (1)..(1326)

97 <400> SEQUENCE: 3

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100 1 5 10 15
102 acc gtt cta ttt ctc ttg ttt cta ttt tct aag gta agt aat gtc act 96
103 Thr Val Leu Phe Leu Leu Phe Leu Phe Ser Lys Val Ser Asn Val Thr
104 20 25 30
106 tta tcg aaa aag gaa tta act ctt ttt tcg ata agc aat ttt ctg ata 144
107 Leu Ser Lys Lys Glu Leu Thr Leu Phe Ser Ile Ser Asn Phe Leu Ile
108 35 40 45
110 atg att gct gtt acg atg gtg aac gta aac ctg ttt tat cct gca gag 192
111 Met Ile Ala Val Thr Met Val Asn Val Asn Leu Phe Tyr Pro Ala Glu
112 50 55 60
114 cct ctt tat ttt ata gct tta tca att tat ctt aat aga cag aat agt 240
115 Pro Leu Tyr Phe Ile Ala Leu Ser Ile Tyr Leu Asn Arg Gln Asn Ser
116 65 70 75 80
118 ctt tct cta aat ata ttt tat ggt ctg ctg cct gtt gcc agt tct gac 288
119 Leu Ser Leu Asn Ile Phe Tyr Gly Leu Leu Pro Val Ala Ser Ser Asp
120 85 90 95
122 ttg ttt agg cgg gca atc ata ttc ttt atc ttg gat gga act caa gga 336
123 Leu Phe Arg Arg Ala Ile Ile Phe Phe Ile Leu Asp Gly Thr Gln Gly
124 100 105 110
126 att gta atg ggc agt agc att ata acc acc tat atg atc gag ttt gca 384
127 Ile Val Met Gly Ser Ser Ile Ile Thr Thr Tyr Met Ile Glu Phe Ala
128 115 120 125
130 gga ata gcg cta agt tac ctc ttt ctc agt gtg ttc aat gtt gat att 432
131 Gly Ile Ala Leu Ser Tyr Leu Phe Leu Ser Val Phe Asn Val Asp Ile
132 130 135 140
134 ggt cga ctt aaa gat agt ttg acc aag atg aag gtc aaa aaa cgc ttg 480
135 Gly Arg Leu Lys Asp Ser Leu Thr Lys Met Lys Val Lys Lys Arg Leu
136 145 150 155 160
138 att cca atg aat att act atg ctt cta tac tac ctt tta ata cag gta 528
139 Ile Pro Met Asn Ile Thr Met Leu Leu Tyr Tyr Leu Leu Ile Gln Val
140 165 170 175
142 ttg tat gtt ata gag agt tat aat gtg ata ccg act tta aaa ttt cgt 576
143 Leu Tyr Val Ile Glu Ser Tyr Asn Val Ile Pro Thr Leu Lys Phe Arg
144 180 185 190
146 aaa ttt gtc gtt att gtc tat ctt att tta ttt ttg att ctg atc tca 624
147 Lys Phe Val Val Ile Val Tyr Leu Ile Leu Phe Leu Ile Leu Ile Ser
148 195 200 205
150 ttt tta agc caa tat acc aaa caa aag gtt caa aat gag ata atg gca 672
151 Phe Leu Ser Gln Tyr Thr Lys Gln Lys Val Gln Asn Glu Ile Met Ala
152 210 215 220
154 caa aag gaa gct cag att cga aat atc acc cag tat agt cag caa ata 720
155 Gln Lys Glu Ala Gln Ile Arg Asn Ile Thr Gln Tyr Ser Gln Gln Ile
156 225 230 235 240
158 gaa tct ctt tac aag gat att cga agt ttc cgc cat gat tat ctg aat 768

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159 Glu Ser Leu Tyr Lys Asp Ile Arg Ser Phe Arg His Asp Tyr Leu Asn
160          245          250          255
162 att tta act agc ctc aga tta ggc att gaa aat aaa gat tta gct agt      816
163 Ile Leu Thr Ser Leu Arg Leu Gly Ile Glu Asn Lys Asp Leu Ala Ser
164          260          265          270
166 att gaa aag att tac cat caa atc tta gaa aaa aca gga cat caa ttg      864
167 Ile Glu Lys Ile Tyr His Gln Ile Leu Glu Lys Thr Gly His Gln Leu
168          275          280          285
170 cag gat acc cgt tat aat atc ggc cat cta gct aat att caa aac gat      912
171 Gln Asp Thr Arg Tyr Asn Ile Gly His Leu Ala Asn Ile Gln Asn Asp
172          290          295          300
174 gct gtc aag ggt atc ttg tca gca aaa atc tta gaa gct cag aat aaa      960
175 Ala Val Lys Gly Ile Leu Ser Ala Lys Ile Leu Glu Ala Gln Asn Lys
176 305          310          315          320
178 aag att gct gtc aat gta gaa gtc tca agt aaa ata caa ctg cct gag      1008
179 Lys Ile Ala Val Asn Val Glu Val Ser Ser Lys Ile Gln Leu Pro Glu
180          325          330          335
182 atg gag ttg ctt gat ttc att acc ata ctt tct atc ttg tgt gat aat      1056
183 Met Glu Leu Leu Asp Phe Ile Thr Ile Leu Ser Ile Leu Cys Asp Asn
184          340          345          350
186 gcc att gag gct gct ttc gaa tca tta aat cct gaa att cag tta gcc      1104
187 Ala Ile Glu Ala Ala Phe Glu Ser Leu Asn Pro Glu Ile Gln Leu Ala
188          355          360          365
190 ttt ttt aag aaa aat ggc agt ata gtc ttt atc att cag aat tcc acc      1152
191 Phe Phe Lys Lys Asn Gly Ser Ile Val Phe Ile Ile Gln Asn Ser Thr
192          370          375          380
194 aaa gaa aaa caa ata gat gtg agt aaa att ttt aaa gaa aac tat tcc      1200
195 Lys Glu Lys Gln Ile Asp Val Ser Lys Ile Phe Lys Glu Asn Tyr Ser
196 385          390          395          400
198 act aaa ggc tcc aat cgc ggt att ggt tta gca aag gtg aat cat att      1248
199 Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile
200          405          410          415
202 ctt gaa cat tat ccc aaa acc agt tta caa aca agc aat cat cat cat      1296
203 Leu Glu His Tyr Pro Lys Thr Ser Leu Gln Thr Ser Asn His His His
204          420          425          430
206 tta ttc aag caa ctc cta ata ata aaa tag      1326
207 Leu Phe Lys Gln Leu Leu Ile Ile Lys
208          435          440
211 <210> SEQ ID NO: 4
213 <211> LENGTH: 441
215 <212> TYPE: PRT
217 <213> ORGANISM: Streptococcus mutans
221 <400> SEQUENCE: 4
223 Met Asn Glu Ala Leu Met Ile Leu Ser Asn Gly Leu Leu Thr Tyr Leu
224 1          5          10          15
227 Thr Val Leu Phe Leu Leu Phe Leu Phe Ser Lys Val Ser Asn Val Thr
228          20          25          30
231 Leu Ser Lys Lys Glu Leu Thr Leu Phe Ser Ile Ser Asn Phe Leu Ile
232          35          40          45

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235 Met Ile Ala Val Thr Met Val Asn Val Asn Leu Phe Tyr Pro Ala Glu
236      50      55      60
239 Pro Leu Tyr Phe Ile Ala Leu Ser Ile Tyr Leu Asn Arg Gln Asn Ser
240 65      70      75      80
243 Leu Ser Leu Asn Ile Phe Tyr Gly Leu Leu Pro Val Ala Ser Ser Asp
244      85      90      95
247 Leu Phe Arg Arg Ala Ile Ile Phe Phe Ile Leu Asp Gly Thr Gln Gly
248      100      105      110
251 Ile Val Met Gly Ser Ser Ile Ile Thr Thr Tyr Met Ile Glu Phe Ala
252      115      120      125
255 Gly Ile Ala Leu Ser Tyr Leu Phe Leu Ser Val Phe Asn Val Asp Ile
256      130      135      140
259 Gly Arg Leu Lys Asp Ser Leu Thr Lys Met Lys Val Lys Lys Arg Leu
260 145      150      155      160
263 Ile Pro Met Asn Ile Thr Met Leu Leu Tyr Tyr Leu Leu Ile Gln Val
264      165      170      175
267 Leu Tyr Val Ile Glu Ser Tyr Asn Val Ile Pro Thr Leu Lys Phe Arg
268      180      185      190
271 Lys Phe Val Val Ile Val Tyr Leu Ile Leu Phe Leu Ile Leu Ile Ser
272      195      200      205
275 Phe Leu Ser Gln Tyr Thr Lys Gln Lys Val Gln Asn Glu Ile Met Ala
276      210      215      220
279 Gln Lys Glu Ala Gln Ile Arg Asn Ile Thr Gln Tyr Ser Gln Gln Ile
280 225      230      235      240
283 Glu Ser Leu Tyr Lys Asp Ile Arg Ser Phe Arg His Asp Tyr Leu Asn
284      245      250      255
287 Ile Leu Thr Ser Leu Arg Leu Gly Ile Glu Asn Lys Asp Leu Ala Ser
288      260      265      270
291 Ile Glu Lys Ile Tyr His Gln Ile Leu Glu Lys Thr Gly His Gln Leu
292      275      280      285
295 Gln Asp Thr Arg Tyr Asn Ile Gly His Leu Ala Asn Ile Gln Asn Asp
296      290      295      300
299 Ala Val Lys Gly Ile Leu Ser Ala Lys Ile Leu Glu Ala Gln Asn Lys
300 305      310      315      320
303 Lys Ile Ala Val Asn Val Glu Val Ser Ser Lys Ile Gln Leu Pro Glu
304      325      330      335
307 Met Glu Leu Leu Asp Phe Ile Thr Ile Leu Ser Ile Leu Cys Asp Asn
308      340      345      350
311 Ala Ile Glu Ala Ala Phe Glu Ser Leu Asn Pro Glu Ile Gln Leu Ala
312      355      360      365
315 Phe Phe Lys Lys Asn Gly Ser Ile Val Phe Ile Ile Gln Asn Ser Thr
316      370      375      380
319 Lys Glu Lys Gln Ile Asp Val Ser Lys Ile Phe Lys Glu Asn Tyr Ser
320 385      390      395      400
323 Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile
324      405      410      415
327 Leu Glu His Tyr Pro Lys Thr Ser Leu Gln Thr Ser Asn His His His
328      420      425      430
331 Leu Phe Lys Gln Leu Leu Ile Ile Lys

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Input Set : A:\SEQUENCE LISTING.txt

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337 <211> LENGTH: 750
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341 <213> ORGANISM: Streptococcus mutans
345 <220> FEATURE:
347 <221> NAME/KEY: CDS
349 <222> LOCATION: (1)..(750)
353 <400> SEQUENCE: 5
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356 1          5          10          15
358 ctt gaa acc acc att gca gct atc atg aaa gaa aaa aat tgg tct tat      96
359 Leu Glu Thr Thr Ile Ala Ala Ile Met Lys Glu Lys Asn Trp Ser Tyr
360          20          25          30
362 aaa gaa ttg act att ttt gga aaa cca caa caa ctt att gac gct atc      144
363 Lys Glu Leu Thr Ile Phe Gly Lys Pro Gln Gln Leu Ile Asp Ala Ile
364          35          40          45
366 cct gaa aag ggc aat cac cag att ttc ttt ttg gat att gaa atc aaa      192
367 Pro Glu Lys Gly Asn His Gln Ile Phe Phe Leu Asp Ile Glu Ile Lys
368          50          55          60
370 aaa gag gaa aag aaa gga ctg gaa gta gcc aat cag att aga cag cat      240
371 Lys Glu Glu Lys Lys Gly Leu Glu Val Ala Asn Gln Ile Arg Gln His
372 65          70          75          80
374 aat cct agt gca gtt att gtc ttt gtc acg aca cat tct gag ttt atg      288
375 Asn Pro Ser Ala Val Ile Val Phe Val Thr Thr His Ser Glu Phe Met
376          85          90          95
378 ccc ctc act ttt cag tat cag gta tct gct ttg gat ttt att gat aaa      336
379 Pro Leu Thr Phe Gln Tyr Gln Val Ser Ala Leu Asp Phe Ile Asp Lys
380          100         105         110
382 tct ttg aat cct gag gag ttc tcc cac cgc att gaa tca gcg ctg tat      384
383 Ser Leu Asn Pro Glu Glu Phe Ser His Arg Ile Glu Ser Ala Leu Tyr
384          115         120         125
386 tat gct atg gaa aac agc cag aag aat ggt caa tca gag gaa ctt ttt      432
387 Tyr Ala Met Glu Asn Ser Gln Lys Asn Gly Gln Ser Glu Glu Leu Phe
388          130         135         140
390 att ttc cat tca tct gaa act cag ttt cag gtc cct ttt gct gag att      480
391 Ile Phe His Ser Ser Glu Thr Gln Phe Gln Val Pro Phe Ala Glu Ile
392 145         150         155         160
394 ctg tat ttt gaa aca tct tca aca gcc cat aag ctc tgc ctt tat act      528
395 Leu Tyr Phe Glu Thr Ser Ser Thr Ala His Lys Leu Cys Leu Tyr Thr
396          165         170         175
398 tat gat gaa cgg att gaa ttc tac ggc agt atg act gac att gtt aaa      576
399 Tyr Asp Glu Arg Ile Glu Phe Tyr Gly Ser Met Thr Asp Ile Val Lys
400          180         185         190
402 atg gat aag aga ctt ttt cag tgc cat cgc tct ttt att gtc aat cct      624
403 Met Asp Lys Arg Leu Phe Gln Cys His Arg Ser Phe Ile Val Asn Pro
404          195         200         205
406 gcc aat att acc cgt att gat cgg aaa aaa cgc ttg gcc tat ttt cga      672

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VERIFICATION SUMMARY

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